

FIGURE 1

1 ATGTCAGTGGGAGCCATGAAGAAGGAGTGGGAGGGCAGTTGGGCTTGGAGGCGGCAGC 60
61 GGCTGCCAGGCTACGGAGGAGACCCCTTCCCGACTGCGGGCTTGCCTCCGGGACAA 120
121 GGTGGCAGGCGCTGGAGGCTGCCGAGCCTGCGTGGGTGGAGGGAGCTCAGCTCGGTG 180
181 TGGGAGCAGGCGACCGGCACTGGCTGGATGGACCTGGAAGCCTCGCTGCTGCCCACTGGT 240
241 CCCAATGCCAGCAACACCTCTGATGGCCCCCGATAACCTCACTTCAGCAGGATCACCTCCT 300
301 CGCACGGGAGCATCTCCTACATCAACATCATGCTTCGGTGTTCGGCACCATCTGC 360
361 CTCCTGGGCATCATCGGGAACCTCCACGGTCATCTTCGCGGTGCGTGAAGAAGTCCAAGCTG 420
421 CACTGGTGCAACAACGTCCCCGACATCTTCATCATCAACCTCTCGGTAGTAGATCTCCTC 480
481 TTTCTCCTGGGCATGCCCTTCATGATCCACCATGGGCAATGGGTGTGGCACTTT 540
541 GGGAGACCATGTGCACCCCTCATCACGGCCATGGATGCCAATAGTCAGTTCACCAAGCAC 600
601 TACATCCTGACCGCCATGGCCATTGACCGCTACCTGGCCACTGTCCACCCCATCTCTCC 660
661 ACGAAGTTCGGAAGCCCTCTGTGGCCACCCCTGGTGATCTGCCCTCCTGTGGGCCCTCTCC 720
721 TTCATCAGCATCACCCCTGTGTGGCTGTATGCCAGACTCATCCCCCTTCCAGGAGGTGCA 780
781 GTGGGCTGCGGCATACGCCCTGCCCAACCCAGACACTGACCTCTACTGTTACCCCTGTAC 840
841 CAGTTTTCCTGGCCTTTGCCCTTGCCCTTTTGTGGTCATCACAGCCGCATACGTGAGGATC 900
901 CTGCAGCGCATGACGTCTCTAGTGGCCCCCGCCTCCAGCGCATCCGGCTGCGGACA 960
961 AAGAGGGTGACCCGCACAGCCATCGCCATCTGTCTGTCTTCTTGTGTGTGGCACCC 1020
1021 TACTATGTGCTACAGCTGACCCAGTTGTCCATCAGCCGCCGACCCCTCACCTTTGTCTAC 1080
1081 TTATACAATGCGGCCATCAGCTTGGGCTATGCCAACAGCTGCCCTCAACCCCTTTGTGTAC 1140
1141 ATCGTGCTCTGTGAGACGTTCCGCAACCGCTTGGTCCGTGCGGTGAAGCCTGCAGCCAG 1200
1201 GGCAGCTTCGCGCTGTACCAACGCTCAGACGGCTGACGAGGAGAGACAGAAAGCAAA 1260
1261 GGCACCTGA 1269

FIGURE 2

1	M	S	V	G	A	T	R	A	S	I	G	V	P	D	I	F	A	N	L	S	V	G	A	V	R	A	C	G	A	S	L	G	P	20
21	G	C	Q	R	A	W	T	N	I	I	N	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	40		
41	G	G	R	A	T	N	I	I	N	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	60				
61	W	E	Q	A	T	N	I	I	N	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	80				
81	P	N	A	S	I	I	N	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	100						
101	R	T	G	S	I	I	N	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	120						
121	L	L	G	S	I	I	N	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	140						
141	H	W	L	C	N	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	160								
161	F	L	L	G	N	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	180								
181	G	E	T	M	C	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	200										
201	Y	I	L	T	A	K	T	I	G	N	S	V	G	A	C	G	A	S	L	G	P	220												
221	-	T	K	I	S	C	F	L	M	T	R	Q	A	E	V	240																		
241	F	I	S	C	F	L	M	T	R	Q	A	E	V	260																				
261	V	G	F	L	M	T	R	Q	A	E	V	280																						
281	Q	F	L	M	T	R	Q	A	E	V	300																							
301	L	Q	R	V	L	A	E	V	320																									
321	K	R	Y	L	A	E	V	340																										
341	Y	Y	N	A	E	V	360																											
361	L	Y	N	A	E	V	380																											
381	I	V	L	A	E	V	400																											
401	G	Q	L	A	E	V	420																											
421	G	T	422																															

FIGURE 4

1 GCAGGGACCTGCACCGGCTGCATGGATCTGCAAAACCTCGTTGCTGTCCACTGGCCCCAA 60
61 TGCCAGCAACATCTCCGATGGCCAGGATAATCTCACATTGCCGGGTACCTCCTCGCAC 120
121 AGGGAGTGTCCTACATCAACATCATATGCCCTTCCGTGTTGGTACCATCTGTCTCCT 180
181 GGGCATCGTGGGAAACTCCACGGTCATCTTTGCTGTGGTGAAGAAGTCCAAGCTACACTG 240
241 GTGCAGCAACGTCCCCGACATCTTCATCATCAACCTCTCTGTGGTGATCTGCTCTTCCT 300
301 GCTGGGCATGCCCTTTCATGATCCACCAGCTCATGGGGAACGGCTCTGGCACCTTTGGGGA 360
361 AACCATGTGCACCCCTCATCACAGCCATGGACGCCAACAGTCAGTTCACCTAGCACCTACAT 420
421 CCTGACTGCCATGACCATTGACCGCTACTTGGCCACCGTCCACCCCATCTCCTCCACCAA 480
481 GTTCCGGAAGCCCTCCATGGCCACCCCTGGTGATCTGCCCTCCTGTGGCGCTCTCCTTCAT 540
541 CAGTATCACCCCTGTGTGGCTCTACGCCAGGCTCATTTCCCTTCCCAGGGGTGCTGTGGG 600
601 CTGTGGCATCCGCCCTGCCAAACCCGGACACTGACCTCTACTGGTTCACCTGTACCAGTT 660
661 TTTCCCTGGCCCTTTGCCCTTCCGTTTGTGGTCATTACCGCCGCATACGTGAAATACTACA 720
721 GCGCATGACGTCTTCGGTGGCCCCAGCCCTCCCAACGCAGCATCCGGCTTCGGACAAAGAG 780
781 GGTGACCCGCACGGCCATTGCCATCTGTCTGGTCTTCTTTGTGTGCTGGGCACCCCTACTA 840
841 TGTGCTGCAGCTGACCCAGCTGTCCATCAGCCGCCCGACCCCTCACGTTTGTCTACTTGTA 900
901 CAACGGGCCATCAGCTTGGGCTATGCTAACAGCTGCCCTGAACCCCTTTGTGTACATAGT 960
961 GCTCTGTGAGACCTTTCGAAACGCTTGGTGTGTGTCAGTGAAGCCTGCAGCCCAGGGGCA 1020
1021 GCTCCGCACGGTCAGCAACGCTCAGACAGCTGATGAGGAGAGGACAGAAAGCAAGGCAC 1080
1081 CTGACAATTCCCCAGTCGCCCTCCAAGTCAGGCCACCCCATCAAAACCGTGGGAGAGATAC 1140
1141 TGAGATTAAACCCAAGGCTACCCCTGGGAGAATGCAGAGGCTGGGGGCTTGTAG 1200
1201 CAACCACATTCCAC 1214

FIGURE 5

1	M	D	L	N	M	F	I	I	L	M	A	N	T	C	I	L	D	I	Q	V	F	A	S	L	S	R	S	L	A	D	
21	Q	D	I	I	I	I	Q	M	A	R	Y	L	V	L	V	A	R	T	Y	P	D	V	P	A	S	L	S	N	V	A	
41	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	
61	V	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	
81	F	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	
101	H	A	M	Q	L	D	L	V	L	A	R	T	Y	P	D	V	P	F	Y	R	C	T	P	P	T						
121	A	R	Y	L	V	L	A	R	T	Y	P	D	V	P	F	Y	R	C	T	P	P	T									
141	R	Y	L	V	L	A	R	T	Y	P	D	V	P	F	Y	R	C	T	P	P	T										
161	T	Y	P	D	V	P	F	Y	R	C	T	P	P	T																	
181	Y	P	D	V	P	F	Y	R	C	T	P	P	T																		
201	P	D	V	P	F	Y	R	C	T	P	P	T																			
221	F	P	A	S	L	S	R	S	L	A	D																				
241	P	A	S	L	S	R	S	L	A	D																					
261	I	C	L	S	R	S	L	A	D																						
281	S	I	S	N	V	A	D																								
301	Y	A	N	V	A	D																									
321	R	L	T																												
341	Q																														

FIGURE 6

IP release in MCH1- and
mock-transfected Cos-7 cells

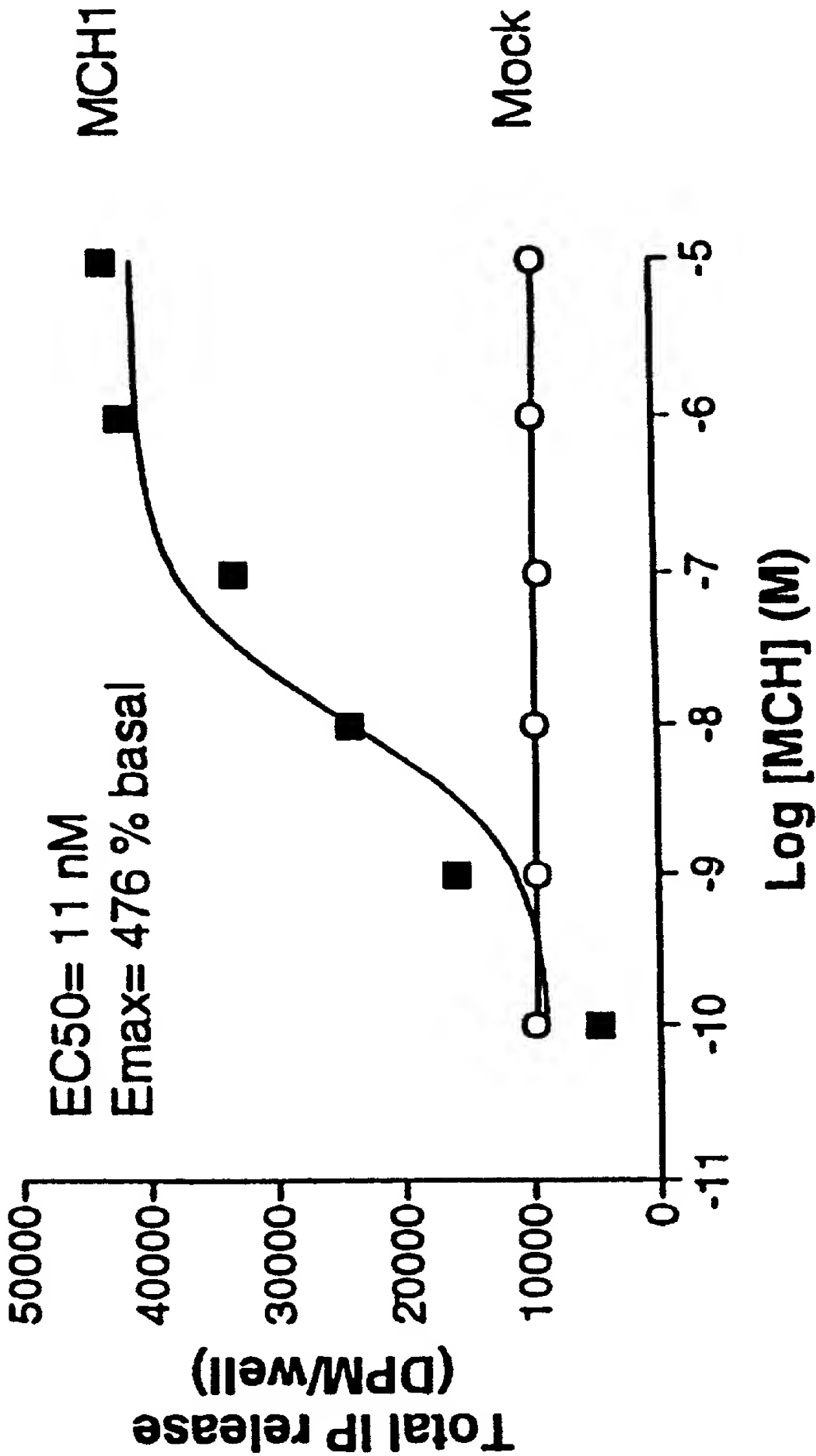


FIGURE 7A

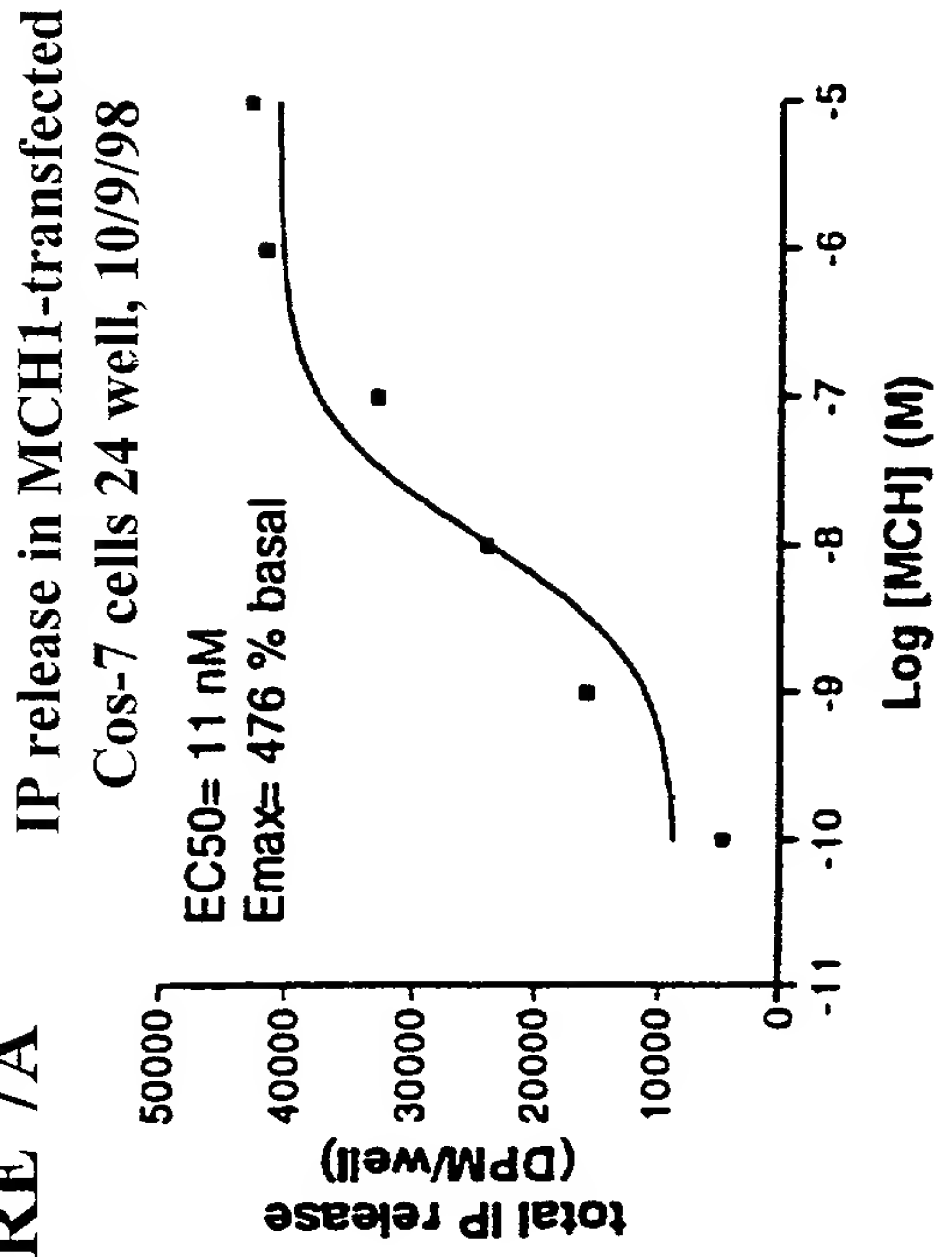


FIGURE 7B

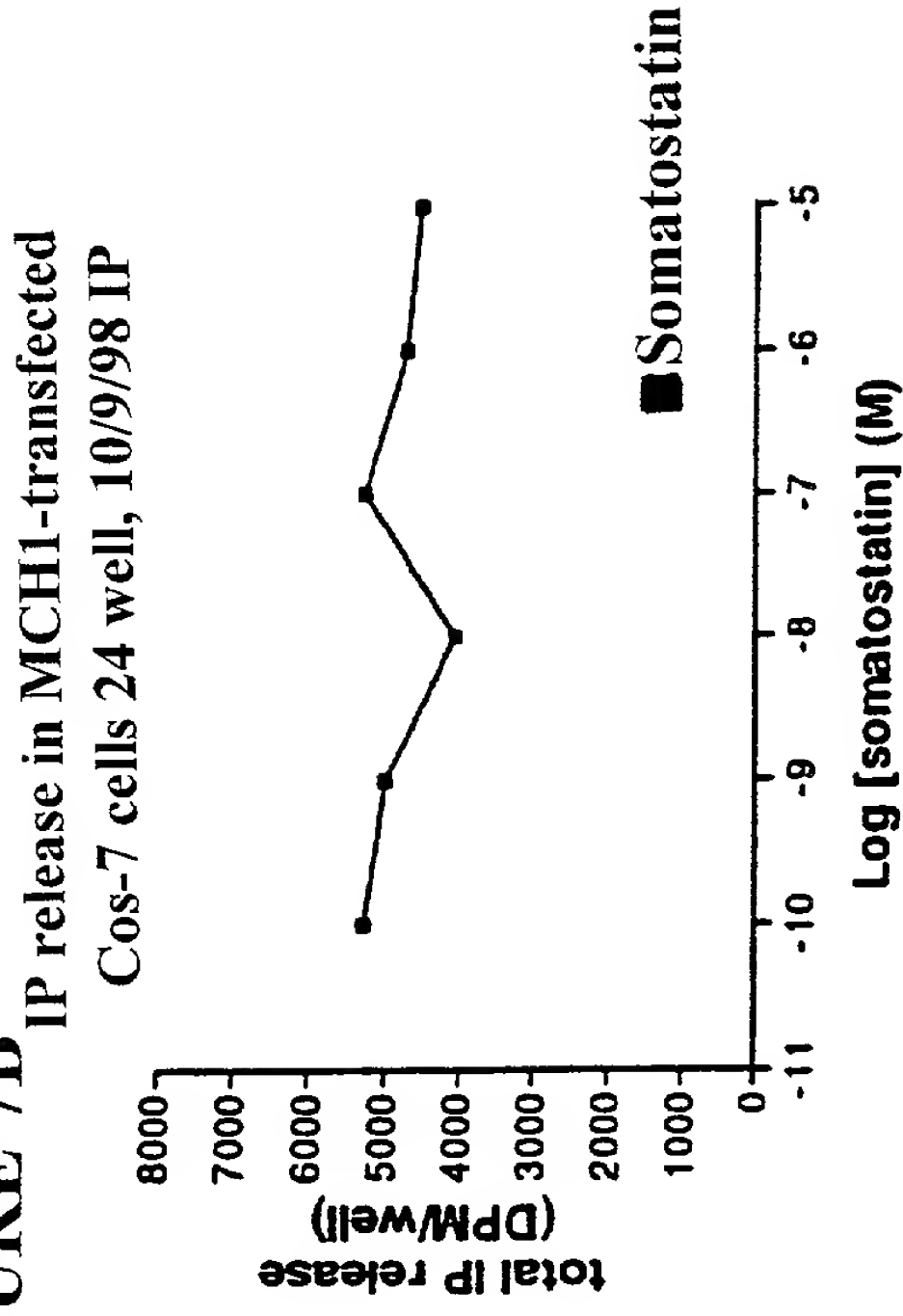


FIGURE 7C

IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98

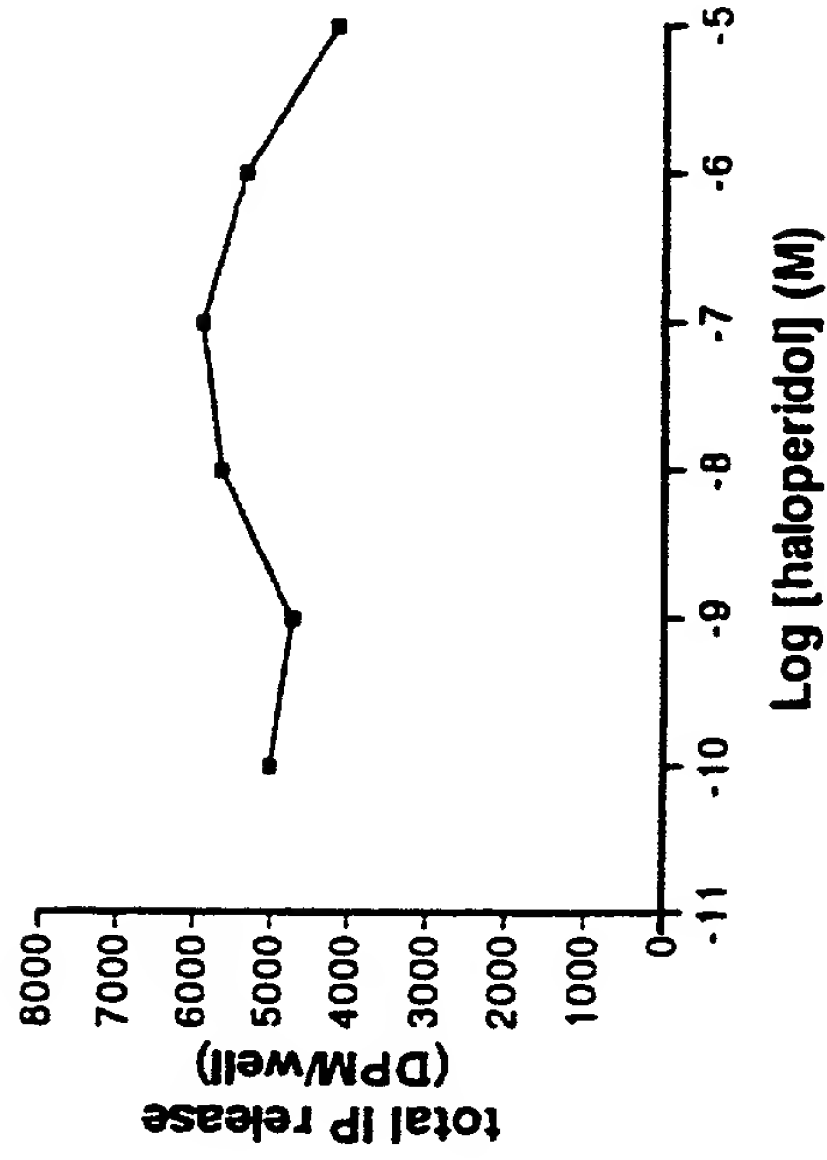


FIGURE 7D

IP release in MCH1-transfected
Cos-7 cells
24 well, 10/9/98

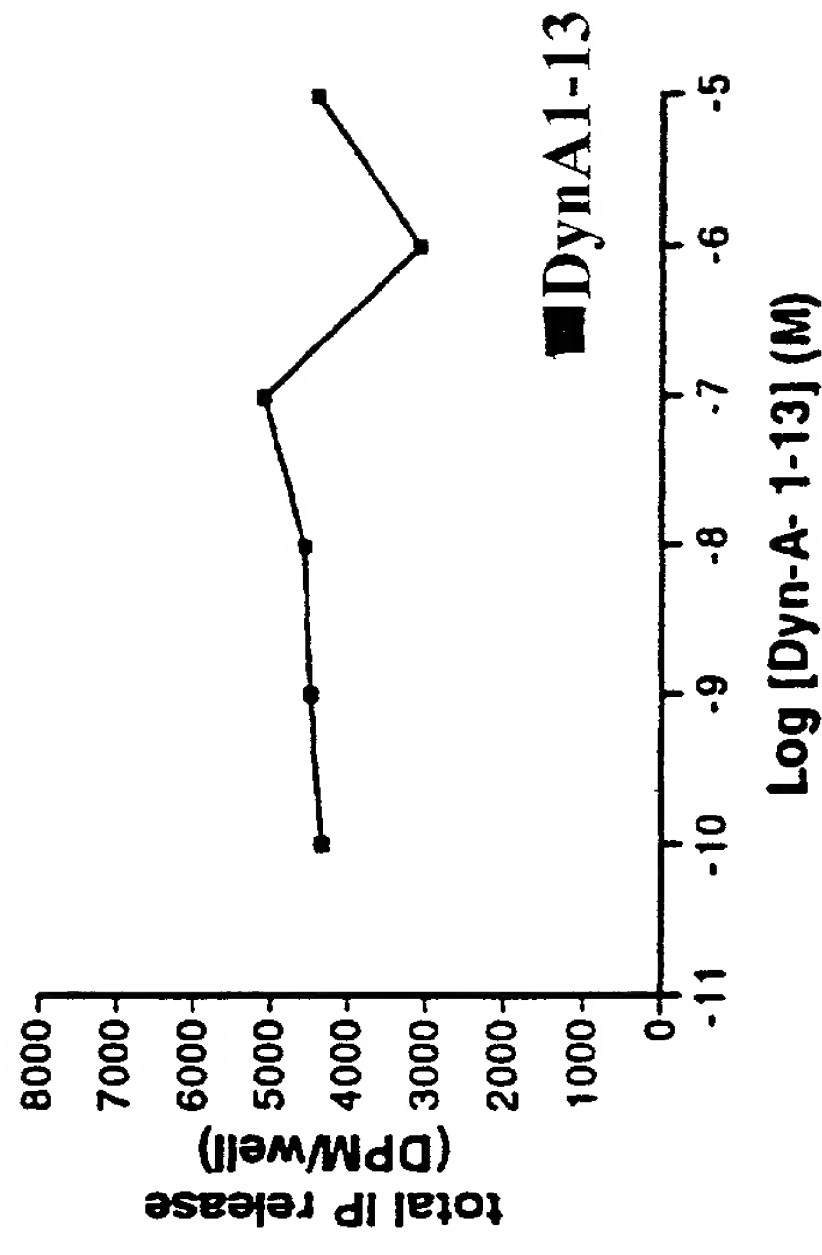


FIGURE 8A

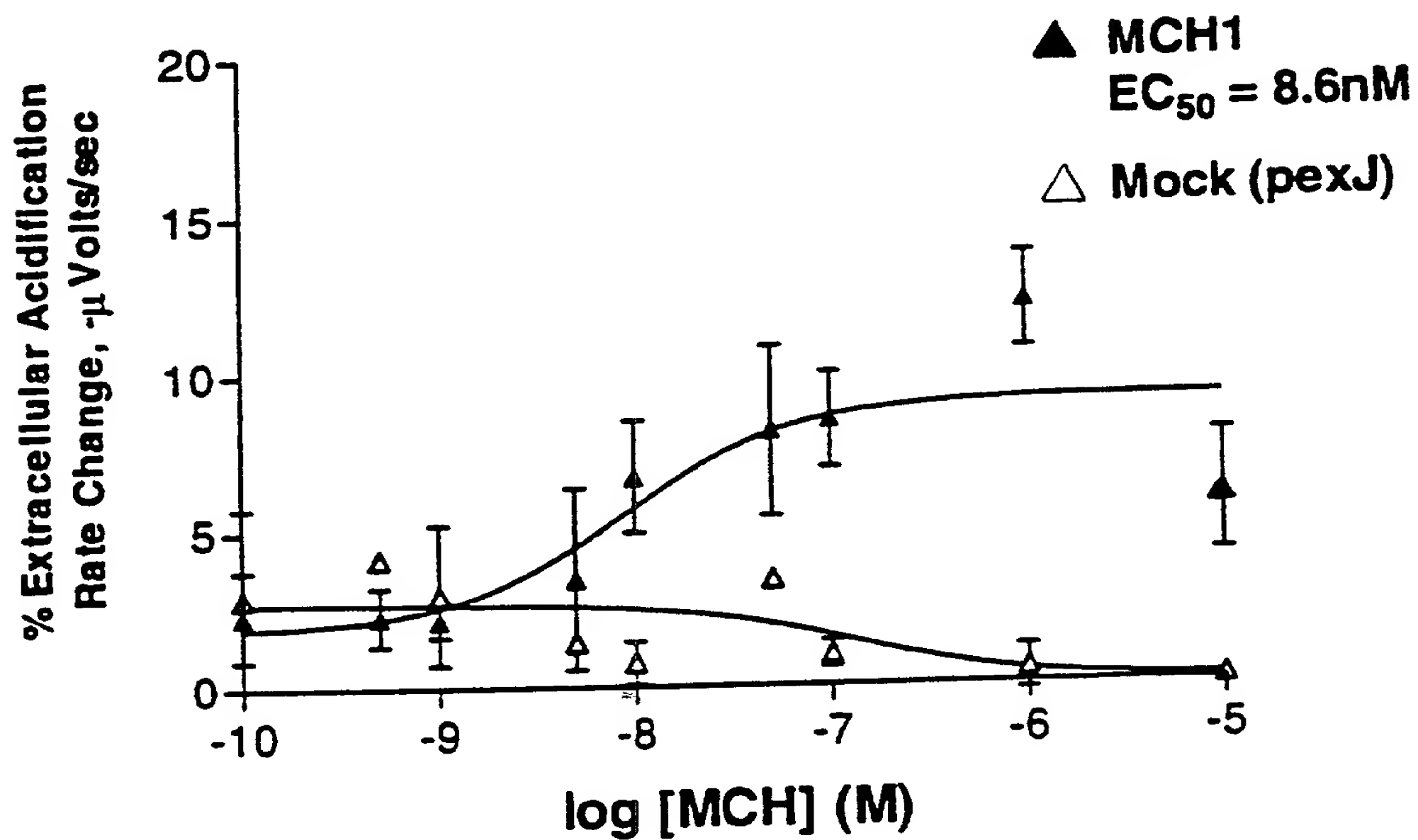
Microphysiometer Response
CHO cells

FIGURE 8B

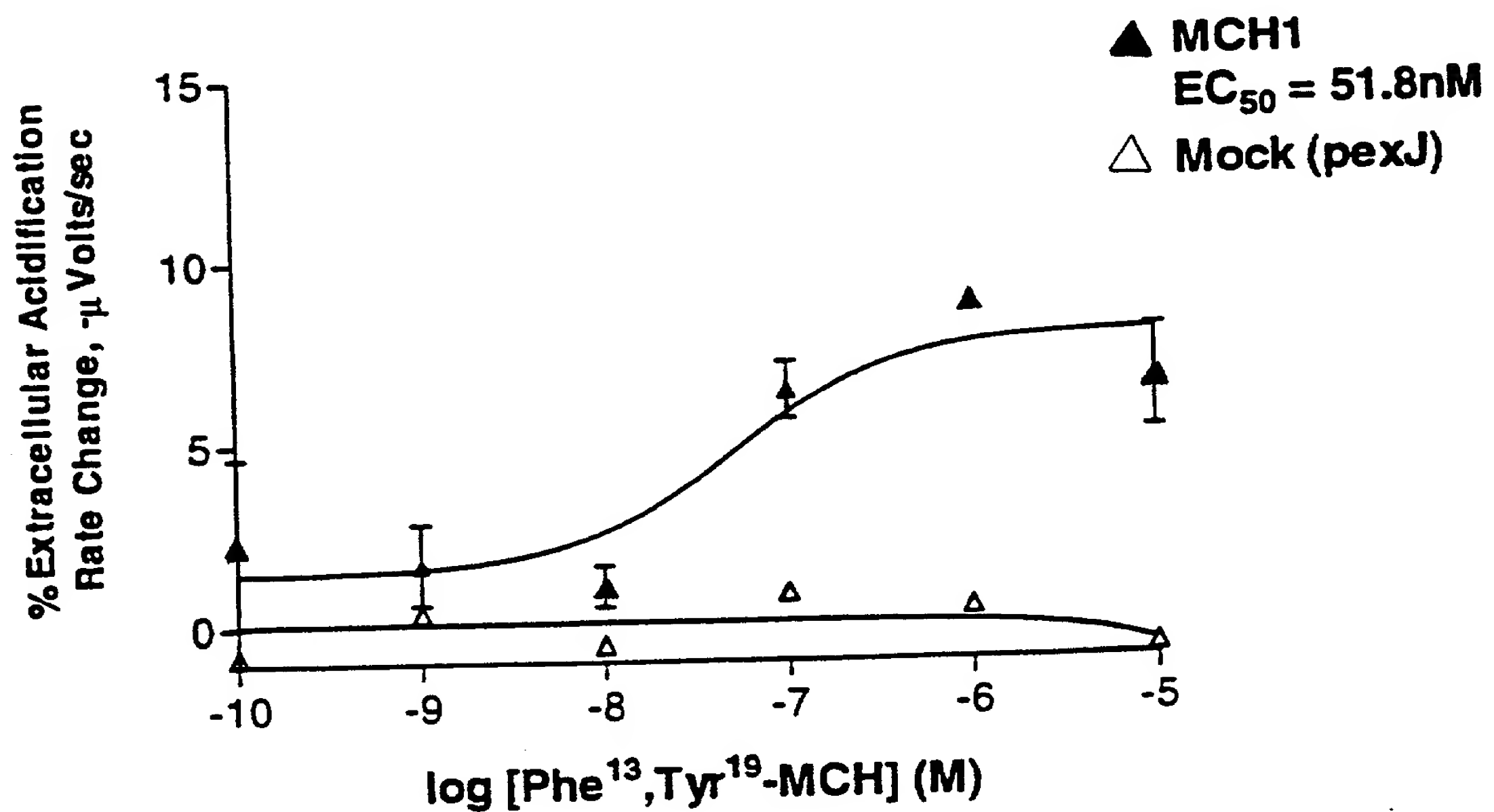
Microphysiometer Response
CHO cells

FIGURE 9

Agonist-Mediated c-fos- β -gal Activity in Cos-7 Cells

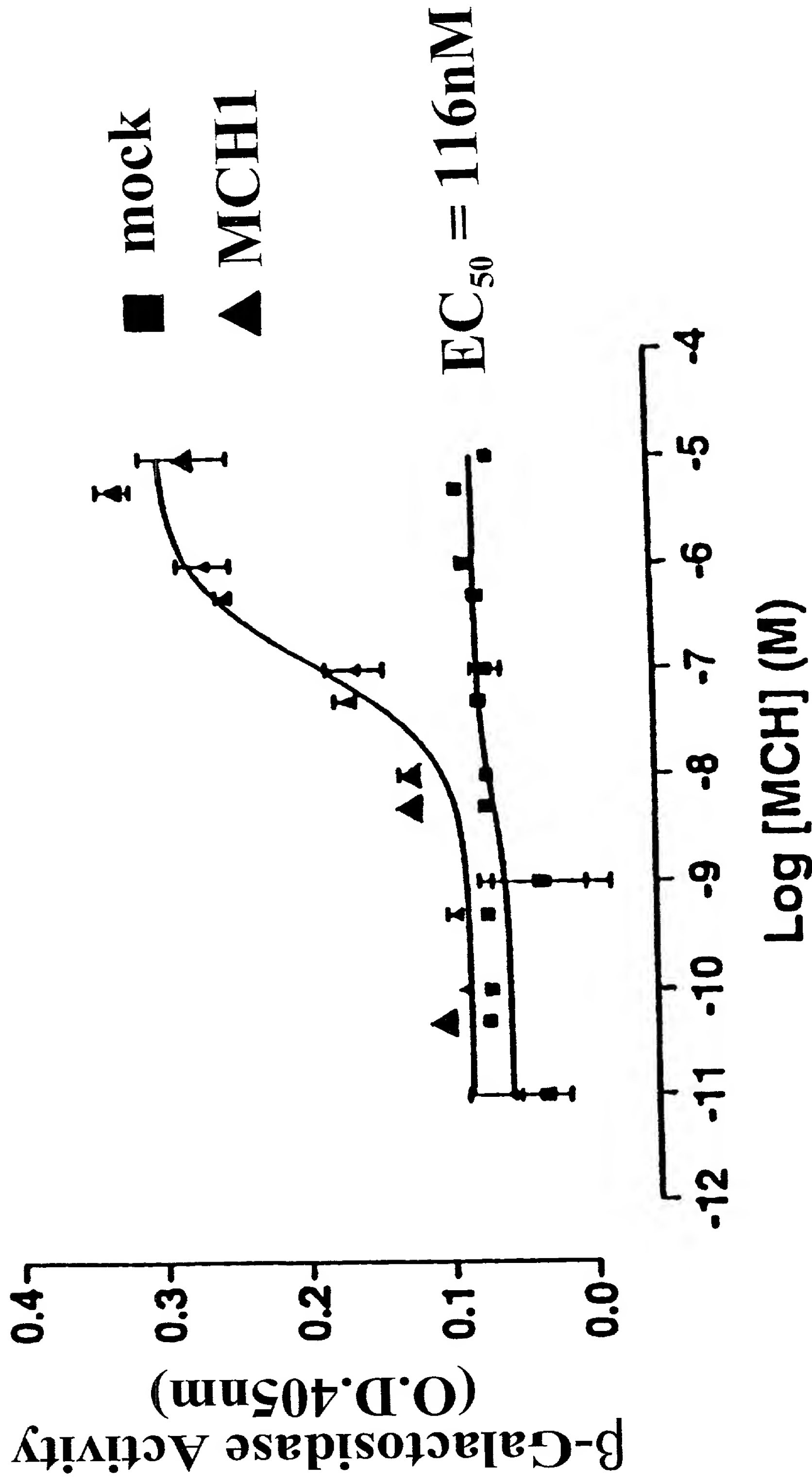


FIGURE 10A

**[125I]Phe13-Tyr19-MCH
binding on transiently
transfected Cos-7 cells**

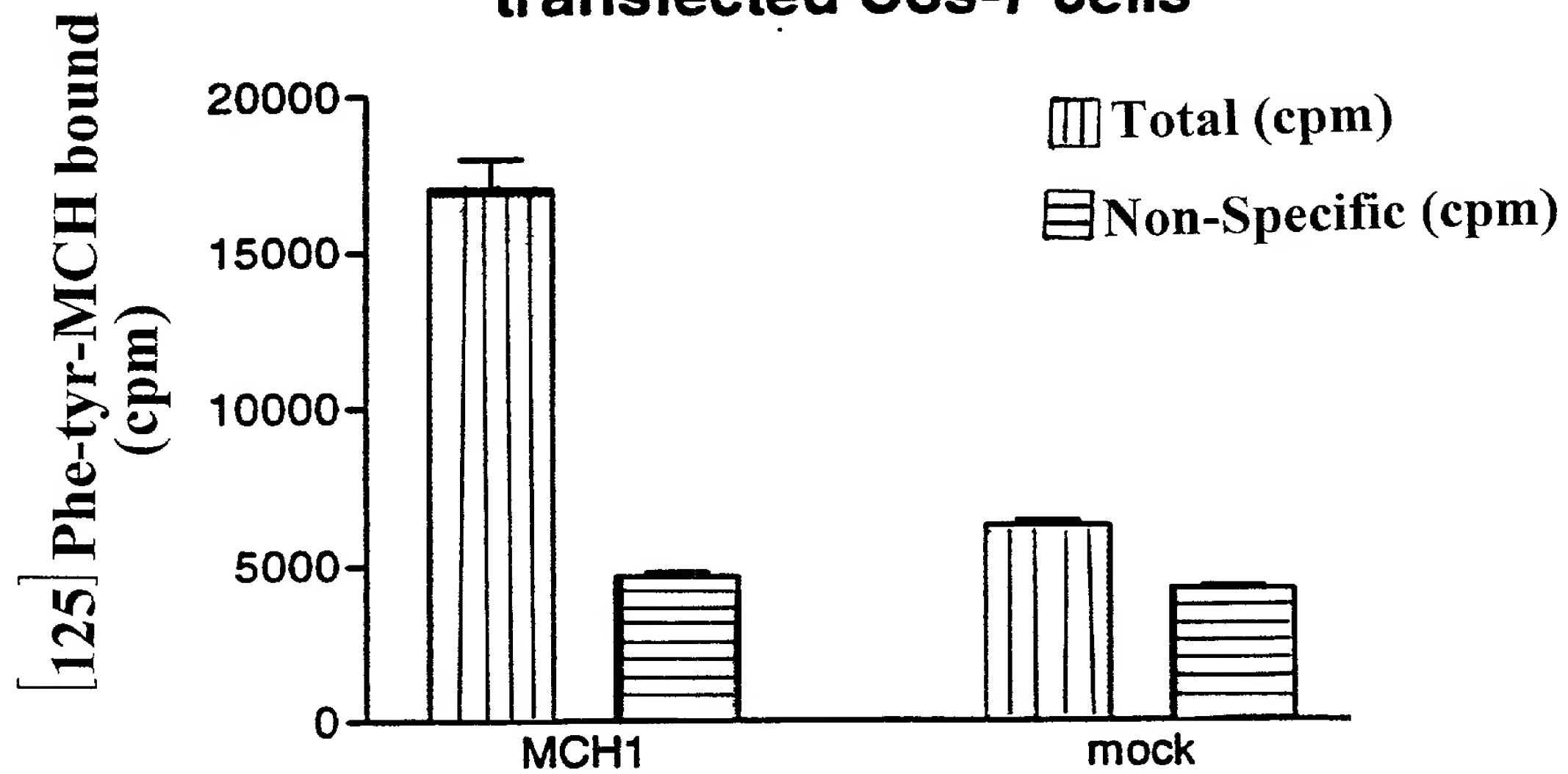


FIGURE 10B

**[125I]Phe13-Tyr19-MCH
binding on transiently
transfected Cos-7 cells**

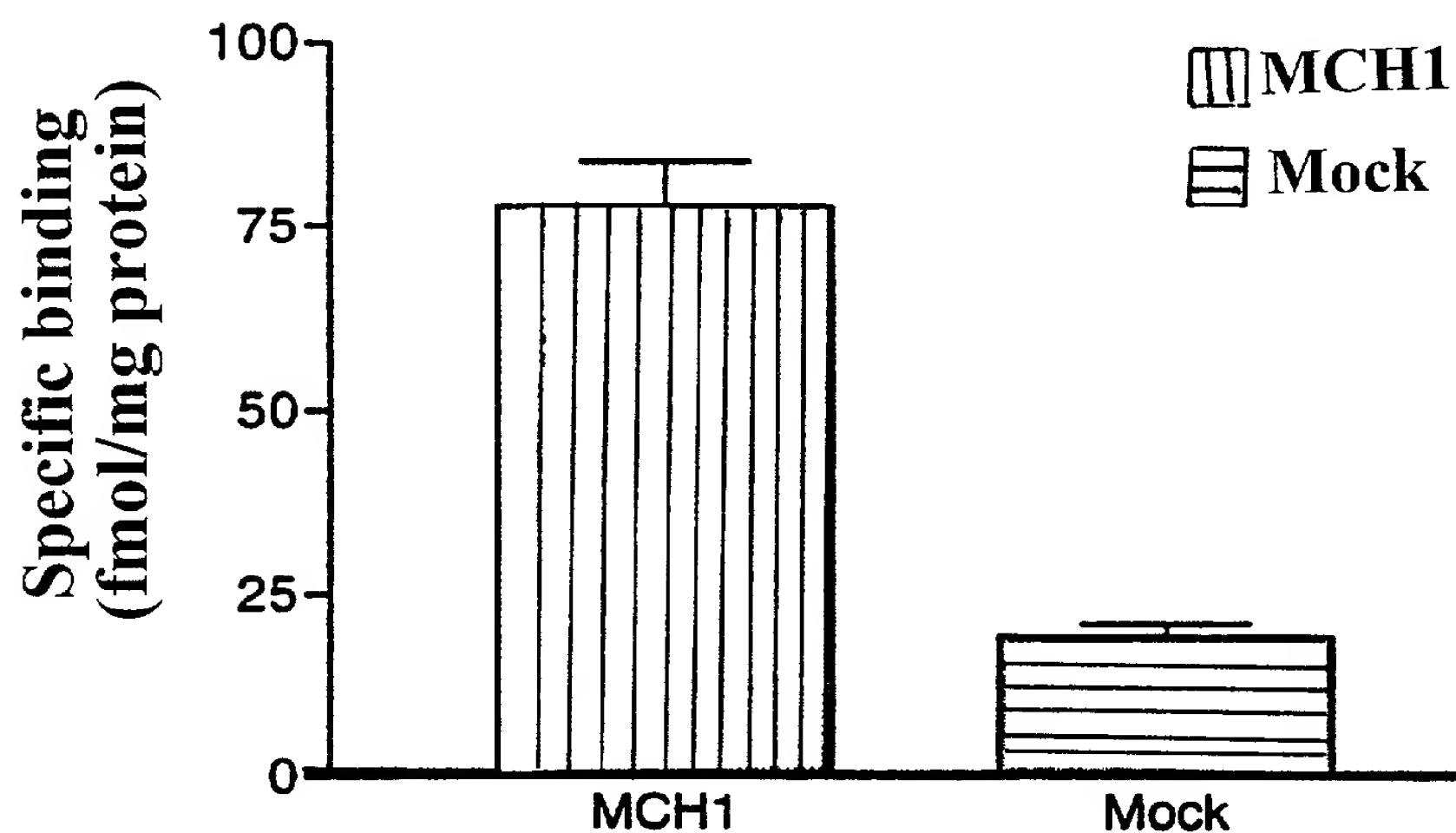


FIGURE 11

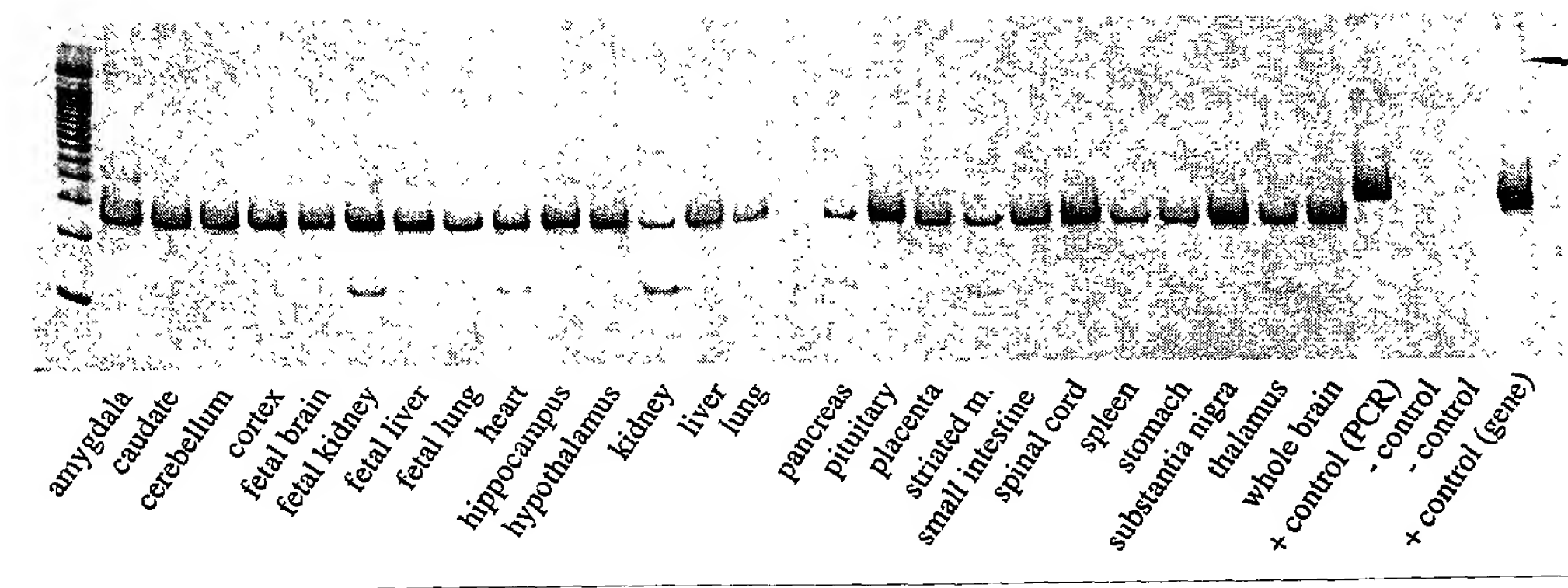


FIGURE 12

TL231	1	MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	40
R106		MSVGAMKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	
R114		MSVGAaKKGV	GRAVGLGGGS	GCQATEEDPL	PDCGACAPGQ	
BO120		~~~~~	~~~~~	~~~~~	~~~~~	

TL231	41	GRRRWRLPQP	AWVEGSSARL	WEQATGTGWM	DLEASLLPTG	80
R106		GRRRWRLPQP	AWVEGSSARL	WEQATGTGwa	DLEASLLPTG	
R114		GRRRWRLPQP	AWVEGSSARL	WEQATGTGwa	DLEASLLPTG	
BO120		~~~~~	~~~~~	~~~~~M	DLEASLLPTG	

TL231	81	PNASNTSDGP	DNLTSA GSPP...	100
R106		PNASNTSDGP	DNLTSA GSPP...	
R114		PNASNTSDGP	DNLTSA GSPP...	
BO120		PNASNTSDGP	DNLTSA GSPP...	

FIGURE 13

1	M	G	G	W	P	R	L	H	F	G	Y	T	F	V	Q	L	K	Y	L	I	G	G
21	S	C	G	E	N	T	L	W	L	E	I	K	I	G	F	Q	R	Y	Y	V	Q	T
41	V	Q	R	Q	A	S	I	N	G	L	T	L	F	S	C	F	R	V	V	N	L	L
61	A	T	W	T	N	I	I	N	M	C	A	K	T	I	A	T	R	Q	A	E	A	
81	M	E	R	G	T	S	G	V	P	T	M	P	P	R	F	S	T	L	I	T	V	
101	K	E	L	T	S	Y	N	P	F	L	A	S	V	L	A	S	A	T	S	F	S	
121	K	D	P	G	D	I	S	D	M	I	I	V	W	P	L	V	I	Q	L	R	N	
141	G	P	Q	W	G	N	T	I	I	T	D	A	L	N	P	A	A	L	G	K	A	
161	V	L	P	A	P	I	V	F	H	A	R	T	Y	P	F	P	I	S	Y	R	Q	
181	G	P	A	D	I	I	I	Q	M	Y	L	A	D	V	A	C	I	A	L	T		
201	R	D	W	L	N	M	F	I	L	D	L	V	R	T	V	S	L	S	N	V	A	
221	A	C	V	E	L	P	A	N	M	A	A	I	L	D	I	Q	V	R	S	L	D	
241	V	G	E	A	T	S	V	L	G	N	T	C	I	L	T	R	F	P	C	S	E	
261	G	A	G	S	S	V	V	S	N	S	V	L	P	Y	A	S	F	T	L	V	E	
281	L	C	S	L	A	F	K	V	V	G	Q	H	L	F	W	A	I	V	L	N	K	R
301	G	A	S	L	G	G	K	V	V	F	P	W	P	F	Y	R	C	T	P	P	T	
321	G	P	A	P	S	T	S	D	W	T	I	A	G	T	V	L	W	F	F	A	E	
341	G	G	R	T	P	I	K	L	H	S	S	L	G	L	R	R	A	V	V	A	S	
361	S	Q	L	G	P	C	L	L	F	T	S	S	A	Y	I	T	P	Y	Y	Q	K	
381																						
401																						
421																						
	20	40	60	80	100	120	140	160	180	200	220	240	260	280	300	320	340	360	380	400	420	422

FIGURE 14

[illegible]

FIGURE 15

